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Engineering Cyclic Tetrapeptides Containing Chimeric Amino Acids as Preferred Reverse-Turn Scaffolds Che, Y.; Marshall, G. R.

J. Med. Chem.; (Article); 2006; 49(1); 111-124. DOI: 10.1021/jm0507072

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Neopetrosiamides, Peptides from the Marine Sponge *Neopetrosia* sp. That Inhibit Amoeboid Invasion by Human Tumor Cells

Williams, D. E.; Austin, P.; Diaz-Marrero, A. R.; Soest, R. V.; Matainaho, T.; Roskelley, C. D.; Roberge, M.; Andersen, R. J.

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Deazapurine Solid-Phase Synthesis: Construction of 3-Substituted Pyrrolo[3,2-d]pyrimidine-6-carboxylates on Cross-Linked Polystyrene Bearing a Cysteamine Linker

Rombouts, F. J. R.; Fridkin, G.; Lubell, W. D.

J. Comb. Chem.; (Article); 2005; 7(4); 589-598. DOI: 10.1021/cc0500021

Abstract Full: HTML / PDF (547k) Supporting Information

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Asymmetric Synthesis of 3-Substituted Proline Chimeras Bearing Polar Side Chains of Proteinogenic Amino Acids

Quancard, J.; Labonne, A.; Jacquot, Y.; Chassaing, G.; Lavielle, S.; Karoyan, P. J. Org. Chem.; (Article); 2004; 69(23); 7940-7948. DOI: 10.1021/jo048762q

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Virtually Complete Control of Simple and Face Diastereoselectivity in the Michael Addition Reactions between Achiral Equivalents of a Nucleophilic Glycine and (S)- or (R)-3-(E-Enoyl)-4-phenyl-1,3-oxazolidin-2-ones: Practical Method for Preparation of  $\beta$ -Substituted Pyroglutamic Acids and Prolines

Soloshonok, V. A.; Ueki, H.; Tiwari, R.; Cai, C.; Hruby, V. J.

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Comparative Assessment of the Ligand and Metal Ion Binding Properties of Integrins $\alpha 9 \beta 1$ and $\alpha 4 \beta 1$

Pepinsky, R. B.; Mumford, R. A.; Chen, L. L.; Leone, D.; Amo, S. E.; Riper, G. V.; Whitty, A.; Dolinski, B.; Lobb, R. R.; Dean, D. C.; Chang, L. L.; Raab, C. E.; Si, Q.; Hagmann, W. K.; Lingham, R. B.
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Doyle, M. P.; Davies, S. B.; May, E. J.
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Rational Design of Highly Diastereoselective, Organic Base-Catalyzed, Room-Temperature Michael Addition Reactions <sup>1</sup>
Soloshonok, V. A.; Cai, C.; Hruby, V. J.; Meervelt, L. V.; Yamazaki, T.
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Bolin, D. R.; Swain, A. L.; Sarabu, R.; Berthel, S. J.; Gillespie, P.; Huby, N. J. S.; Makofske, R.; Orzechowski, L.; Perrotta, A.; Toth, K.; Cooper, J. P.; Jiang, N.; Falcioni, F.; Campbell, R.; Cox, D.; Gaizband, D.; Belunis, C. J.; Vidovic, D.; Ito, K.; Crowther, R.; Kammlott, U.; Zhang, X.; Palermo, R.; Weber, D.; Guenot, J.; Nagy, Z.; Olson, G. L.

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Tong, Y.; Fobian, Y. M.; Wu, M.; Boyd, N. D.; Moeller, K. D.

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Sternfeld, F.; Guiblin, A. R.; Jelley, R. A.; Matassa, V. G.; Reeve, A. J.; Hunt, P. A.; Beer, M. S.; Heald, A.; Stanton, J. A.; Sohal, B.; Watt, A. P.; Street, L. J.

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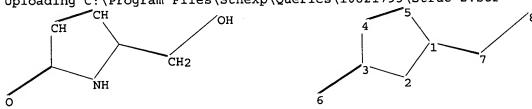
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                                                                  1 ANSWERS
                   43131 ITERATIONS
100.0% PROCESSED
SEARCH TIME: 00.00.01
L3
              1 SEA SSS FUL L1
=> d hitstr
'HITSTR' IS NOT A VALID FORMAT FOR FILE 'REGISTRY'
The following are valid formats:
Substance information can be displayed by requesting individual
fields or predefined formats. The predefined substance formats
are: (RN = CAS Registry Number)
REG
       - Index Name, MF, and structure - no RN
SAM
       - All substance data, except sequence data
FIDE
```

- FIDE, but only 50 names

- Protein sequence data, includes RN

SQIDE3 - Same as SQIDE, but 3-letter amino acid codes are used

SQIDE - IDE, plus sequence data

SOD

#### Page 41

- Same as SQD, but 3-letter amino acid codes are used SOD3 - Protein sequence name information, includes RN SON CALC - Table of calculated properties EPROP - Table of experimental properties - EPROP and CALC PROP Any CA File format may be combined with any substance format to obtain CA references citing the substance. The substance formats must be cited first. The CA File predefined formats are: ABS -- Abstract APPS -- Application and Priority Information

BIB -- CA Accession Number, plus Bibliographic Data

CAN -- CA Accession Number

CBIB -- CA Accession Number, plus Bibliographic Data (compressed)

IND -- Index Data

IPC -- International Patent Classification

PATS -- PI, SO

STD -- BIB, IPC, and NCL

IABS -- ABS, indented, with text labels IBIB -- BIB, indented, with text labels

ISTD -- STD format, indented

OBIB ----- AN, plus Bibliographic Data (original) OIBIB ----- OBIB, indented with text labels

SBIB ----- BIB, no citations SIBIB ----- IBIB, no citations

The ALL format gives FIDE BIB ABS IND RE, plus sequence data when it is available.

The MAX format is the same as ALL.

The IALL format is the same as ALL with BIB ABS and IND indented, with text labels.

For additional information, please consult the following help messages:

HELP DFIELDS -- To see a complete list of individual display fields. HELP FORMATS -- To see detailed descriptions of the predefined formats. ENTER DISPLAY FORMAT (IDE): rn sam 'SAM' IS NOT A VALID FORMAT FOR FILE 'REGISTRY'

The following are valid formats:

Substance information can be displayed by requesting individual fields or predefined formats. The predefined substance formats (RN = CAS Registry Number)

- RN REG

- Index Name, MF, and structure - no RN SAM - All substance data, except sequence data FIDE

- FIDE, but only 50 names SQIDE - IDE, plus sequence data

SQIDE3 - Same as SQIDE, but 3-letter amino acid codes are used

- Protein sequence data, includes RN SQD

- Same as SQD, but 3-letter amino acid codes are used SQD3

- Protein sequence name information, includes RN SON

- Table of calculated properties CALC EPROP - Table of experimental properties

#### PROP - EPROP and CALC

Any CA File format may be combined with any substance format to obtain CA references citing the substance. The substance formats must be cited first. The CA File predefined formats are:

ABS -- Abstract

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OBIB ----- AN, plus Bibliographic Data (original) OIBIB ----- OBIB, indented with text labels

SBIB ----- BIB, no citations SIBIB ----- IBIB, no citations

The ALL format gives FIDE BIB ABS IND RE, plus sequence data when it is available.

The MAX format is the same as ALL.

The IALL format is the same as ALL with BIB ABS and IND indented, with text labels.

For additional information, please consult the following help messages:

HELP DFIELDS -- To see a complete list of individual display fields.
HELP FORMATS -- To see detailed descriptions of the predefined formats.
ENTER DISPLAY FORMAT (IDE):d rn sam
'SAM' IS NOT A VALID FORMAT FOR FILE 'REGISTRY'
'D' IS NOT A VALID FORMAT FOR FILE 'REGISTRY'

The following are valid formats:

Substance information can be displayed by requesting individual fields or predefined formats. The predefined substance formats are: (RN = CAS Registry Number)

REG - RN

SAM - Index Name, MF, and structure - no RN FIDE - All substance data, except sequence data

IDE - FIDE, but only 50 names SQIDE - IDE, plus sequence data

SQIDE3 - Same as SQIDE, but 3-letter amino acid codes are used

SQD - Protein sequence data, includes RN

SQD3 - Same as SQD, but 3-letter amino acid codes are used

SQN - Protein sequence name information, includes RN

CALC - Table of calculated properties EPROP - Table of experimental properties

PROP - EPROP and CALC

Any CA File format may be combined with any substance format to obtain CA references citing the substance. The substance formats

#### Page 43

must be cited first. The CA File predefined formats are:

ABS -- Abstract

APPS -- Application and Priority Information

BIB -- CA Accession Number, plus Bibliographic Data

CAN -- CA Accession Number

CBIB -- CA Accession Number, plus Bibliographic Data (compressed)

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IABS -- ABS, indented, with text labels IBIB -- BIB, indented, with text labels

ISTD -- STD format, indented

OBIB ----- AN, plus Bibliographic Data (original)

OIBIB ----- OBIB, indented with text labels

SBIB ----- BIB, no citations SIBIB ----- IBIB, no citations

The ALL format gives FIDE BIB ABS IND RE, plus sequence data when it is available.

The MAX format is the same as ALL.

The IALL format is the same as ALL with BIB ABS and IND indented, with text labels.

For additional information, please consult the following help messages:

HELP DFIELDS -- To see a complete list of individual display fields. HELP FORMATS -- To see detailed descriptions of the predefined formats. ENTER DISPLAY FORMAT (IDE):sam

L3 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2006 ACS on STN

MF C9 H13 N O4

Absolute stereochemistry. Rotation (-).

\*\*PROPERTY DATA AVAILABLE IN THE 'PROP' FORMAT\*\*

=> d l1

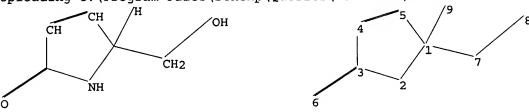
L1 HAS NO ANSWERS

L1 STR

#### Page 44

Structure attributes must be viewed using STN Express query preparation.

=> Uploading C:\Program Files\Stnexp\Queries\10821793\Struc 3.str



chain nodes:
6 7 8 9
ring nodes:
1 2 3 4 5
chain bonds:
1-7 1-9 3-6 7-8
ring bonds:
1-2 1-5 2-3 3-4 4-5
exact/norm bonds:
1-2 1-5 2-3 3-4 3-6 4-5
exact bonds:
1-7 1-9 7-8

Match level:
1:Atom 2:Atom 3:Atom 4:Atom 5:Atom 6:CLASS 7:CLASS 8:CLASS 9:CLASS

#### L4 STRUCTURE UPLOADED

=> d 14 L4 HAS NO ANSWERS L4 STR

Structure attributes must be viewed using STN Express query preparation.

=> 14

SAMPLE SEARCH INITIATED 11:22:00 FILE 'REGISTRY' SAMPLE SCREEN SEARCH COMPLETED - 2128 TO ITERATE

2000 ITERATIONS 94.0% PROCESSED

0 ANSWERS

INCOMPLETE SEARCH (SYSTEM LIMIT EXCEEDED)

SEARCH TIME: 00.00.01

FULL FILE PROJECTIONS: ONLINE \*\*COMPLETE\*\*
BATCH \*\*COMPLETE\*\*

PROJECTED ITERATIONS:

39793 TO 45327

PROJECTED ANSWERS:

0 TO 0

0 SEA SSS SAM L4 L5

=> 14 full

FULL SEARCH INITIATED 11:22:07 FILE 'REGISTRY'

FULL SCREEN SEARCH COMPLETED - 43131 TO ITERATE

100.0% PROCESSED 43131 ITERATIONS

0 ANSWERS

SEARCH TIME: 00.00.01

0 SEA SSS FUL L4 L6

=> log y

COST IN U.S. DOLLARS

SINCE FILE TOTAL ENTRY SESSION

336.58 336.79 FULL ESTIMATED COST

STN INTERNATIONAL LOGOFF AT 11:22:44 ON 05 JAN 2006